

#1

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## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using [BLAST](#) engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)  
**Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix Parameters used in [BLASTN](#) program only:Reward for a match:  Penalty for a mismatch: ☐ Use [Mega BLAST](#) Strand option  View option Masking character option  Masking color option ☐ Show CDS translationOpen gap  and extension gap  penaltiesgap x\_dropoff  expect  word size  Filter ☒ 

Sequence 1

Enter accession, GI or sequence in FASTA format from:  to: 

```
gtgaacttttatgggaaggatgcttctgaaaaacaaatgacagaaaactctccgccaggg
gaatttttttctcaattttgatgaataagaacgatttgaaaatacaatgggtgtgtgtttt
tatcttttttagagagctaaagggtgcctagaatctcttttcaaaaagcagattctctcatg
ttttttttctttatttgttgtcatattctttttacatcttctgaccacttatcctcaagt
tgtacctctcatgttttataatgacaagctggatcaacatgggaaaagggtgaactggca
gtgatttcaccagccctgacatccttgcattccaccagcgtgctcctttaagttcagcca
```

or upload FASTA file  

Sequence 2

Enter accession, GI or sequence in FASTA format from:  to: 

```
gcaatattaacaggcagctgtcccctggcttcccagatgctgggatgactcgcatgtgctg
agcgggtgtggtcactgcaaaggaatgaccctctcacatttcttctgattcgcatagc
cgcgccagcttgtcatctccctcttgggcttcccagacactaagtctggaatgaaaatt
cacctgcttctgaattggccactgggtgggggcaggggtgtgacttggttcccaggctgg
aagattatctcaccagccctagctatataacgggctgggtgtggaggggctccacagggc
cagttccaggggttcatccacaagagagaaaaacata
```

or upload FASTA file   [Comments and suggestions to blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

PubMed

Entrez

## BLAST

OMIM

## Taxonomy

## Structure

**BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]**

Match:  Mismatch:  gap open:  gap extension:

x\_dropoff: 50 expect: 10.000 wordsize: 11 Filter ☒ View option Standard 

Masking character option **X for protein, n for nucleotide** Masking color option **Black**

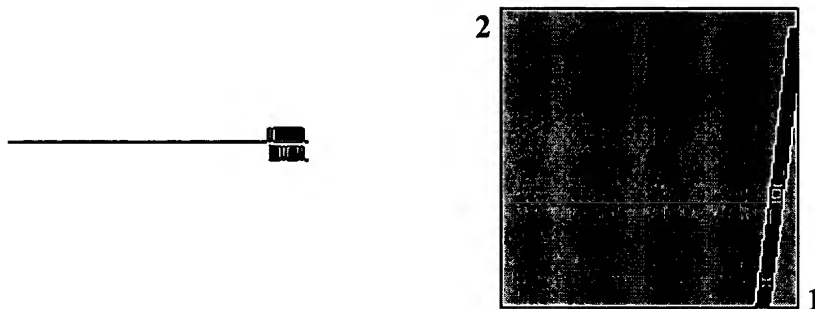
☐ Show CDS translation Align

**Sequence 1: lcl|1\_seq\_1**

Length = 2740 (1 .. 2740)

**Sequence 2: lcl|2\_seq\_2**

Length = 337 (1 .. 337)



**NOTE:**Bitscore and expect value are calculated based on the size of the nr database.

**NOTE:**If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 262 bits (136), Expect = 6e-66  
Identities = 266/321 (82%), Gaps = 7/321 (2%)  
Strand=Plus/Plus

[illegible]

```

Sbjct  121  CGC--GGCCAGCTTGTCATC---TCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGA  175
Query  2581  AAATTCACCTGCCTCTGAGTTGGCTCCTAATGGGGGCGGGAGTGTACTTCGGTTCCCAG  2640
          ||||||||||||||||| |||||  ||  ||||||||| ||  ||||| ||||| |||||
Sbjct  176  AAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGCAGGGGTGTGACTTGGCTTCCCAG  235
Query  2641  GTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGGGGCCAG  2700
          | ||||||||||||||||||| ||||| ||||||||| | | ||||||||||||| |
Sbjct  236  GCTGGAAGATTATCTCACCCAGCCCTAGCTATATAA-CGGGCTGGTGTGGAGGGGCTCCA  294
Query  2701  CAGGGCCAACCTCCAGGGATTC  2721
          |||||||  ||||||| |||
Sbjct  295  CAGGGCCAGTTCCAGGGGTTC  315

```

CPU time: 0.02 user secs. 0.00 sys. secs 0.02 total secs.

Lambda	K	H
1.33	0.621	1.12

## Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Sequences: 1  
 Number of Hits to DB: 30  
 Number of extensions: 5  
 Number of successful extensions: 5  
 Number of sequences better than 10.0: 1  
 Number of HSP's gapped: 2  
 Number of HSP's successfully gapped: 1  
 Length of query: 2740  
 Length of database: 18,315,253,495  
 Length adjustment: 27  
 Effective length of query: 2713  
 Effective length of database: 18,315,253,468  
 Effective search space: 49689282658684  
 Effective search space used: 49689282658684  
 X1: 11 (21.1 bits)  
 X2: 26 (50.0 bits)  
 X3: 26 (50.0 bits)  
 S1: 11 (21.8 bits)  
 S2: 22 (43.0 bits)

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Sequence 1

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```
gtgaacttttatgggaaggatgcttctgaaaaacaaatgacagaaaactctccgccaggg
gaatttttttctcaattttgatgaataagaacgatttgaaaatacaatgggtgtgtgttt
tatcttttagagagctaaaggtgcctagaatctctttcaaaaagcagattctctcatg
tttttttctttatttgttgcataattcttttacatctcttgaccacttatcctcaagt
tgtacctctcatgttttataatgacaagctggatcaacatgggaaaagggtgaactggca
gtgatttcaccagccctgacatccttgcatccaccagcgtgctcctttaagttcagccca
```

or upload FASTA file  

Sequence 2

Enter accession, GI or sequence in FASTA format from:  to: 

```
ggatcctttcatgtttaacaatatcaaccctaaccgaagggaacagcctgcctgacagt
ggctttgccaccatgaataacttcttagtctagtcggttgtaaactcagcccatccca
acacttctgcaagcccatcctctacaaggtgctcattgggaatttcttgagcttctct
ttcaggatcagcctgattctagggcagcagttctcaacctgggggcctcgaccctttgg
gggaatcaaacgaccctttacaggggtcacatatcatctatctatatgtcaggtattta
cattacgattcgtaacagtagcaaaattacaggtatgaaatagcaatgaaataattttat
```

or upload FASTA file   [Comments and suggestions to blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

PubMed

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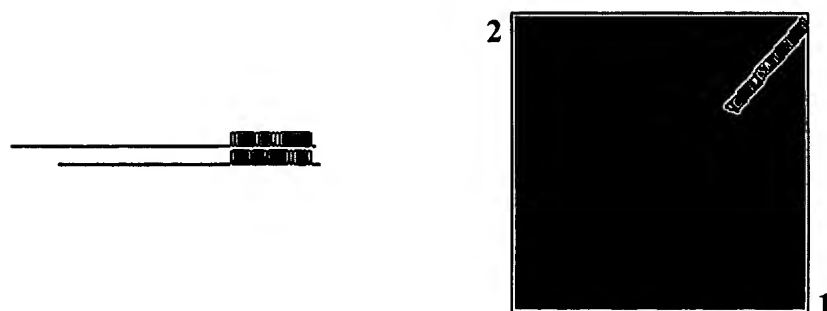
Structure

### BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☒ View option   
 Masking character option  Masking color option   
☐ Show CDS translation

Sequence 1: lcl|1\_seq\_1  
 Length = 2740 (1 .. 2740)

Sequence 2: lcl|2\_seq\_2  
 Length = 2358 (1 .. 2358)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.



Score = 417 bits (217), Expect = 8e-113  
 Identities = 561/699 (80%), Gaps = 20/699 (2%)  
 Strand=Plus/Plus

Query	2034	TTTAGAACACGGTAAGCATGTCATGTGCTAAT---GGCCAGTGACATCATAAAAGAAAAG	2090
Sbjct	1597	TTTAGAACACGGTGAGCCTGTGGTGCACTAATTATGGCCAGTGACACCATAGAGTCAAAG	1656
Query	2091	TGCATTACTGAATGCTTTCAATTTCTTATAATGATGGTAAGGTGGCATGTCATGGGGCCT	2150
Sbjct	1657	TGCATTACTGAATGCTTTCAATTTCTCCTAATGCTGGTACGATGGCATGTCACAGGGCCA	1716
Query	2151	ATTTAGCCCCAGACATCACTCCAAAGAATTCCAAACAGATATAGACAAGTGCCTTTAGGG	2210

9/25/06

Length of database: 18,315,253,495  
Length adjustment: 27  
Effective length of query: 2713  
Effective length of database: 18,315,253,468  
Effective search space: 49689282658684  
Effective search space used: 49689282658684  
X1: 11 (21.1 bits)  
X2: 26 (50.0 bits)  
X3: 26 (50.0 bits)  
S1: 14 (27.6 bits)  
S2: 22 (43.0 bits)